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BFM-SI: A NEW IMPLEMENTATION OF THE BIOGEOCHEMICAL FLUX MODEL IN SEA ICE

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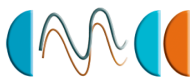
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SUMMARY This work describes a novel implementation of the Biogeochemical Flux Model (BFM) in a sea ice system (BFM-SI). The chosen representative groups of the sea ice food web rely on the same dynamics as the BFM. The main differences between BFM and BFM-SI stand in the type and number of functional groups, in the parameters assigned to several physiological and ecological processes and in the dimensional size classes they represent. The differential equations of BFM-SI are written here according to the nomenclature associated to the new sea ice state variables. At the boundaries, the sea ice system is also coupled to the atmosphere and to the ocean through the exchange of organic and inorganic matter. This is done by computing the entrapment of particulate and dissolved matter and gases when sea ice grows and release to the ocean when sea ice melts to ensure mass conservation. The implementation of the BFM in sea ice and the coupling structure in General Circulation Models will add a new component that may provide new adequate estimate of the role and importance of sea ice biogeochemistry in the global carbon cycle.

Keywords: biogeochemical model, sea ice ecosystem



SEA ICE BIOLOGY IN THE CLIMATE SYSTEM

Though sea ice is only a very thin layer between the ocean and the atmosphere, it plays an important role in the Earth's climate system. The high albedo and its positive feedback, the strong insulating effect, the physical barrier that it creates between the atmosphere and the ocean and its impact on the large-scale thermohaline structure of water masses make sea ice an active component of the climate system. It is thus likely that sea ice acts as a very sensitive indicator of global climate change [12] and has become one of the component which is most studied in the past, present and future climate.

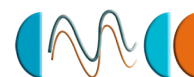
Sea ice is a rich habitat for microbial community. The most abundant species found are unicellular microalgae, mostly diatoms. When sea ice forms, many organisms are either passively or actively entrapped in the salty brines. Their rate of survival in the new habitat depends on their adaptation and/or acclimation to the new environmental conditions (low temperature, high salinity and low light intensities) and on the external supply of nutrients and gases from seawater. Some organisms may die in isolated brines, some may survive or encyst, some may find a favorable habitat and actively grow. Concentrations up to 1000 mg m^{-3} of diatom chlorophyll have been found in Antarctic sea ice [31].

The sea ice biogeochemical cycle is also strongly related to its oceanic counterpart. This is of extreme biological importance at the end of the ice season, when sea ice starts melting and a sea ice algae bloom occurs. The fate of this biomass depends on the rate of melting and on the vertical stability of the water column. If the stratification is high and the rate of melting is low, sea ice algae may stay long time in the upper part of the water column and may seed a pelagic phytoplankton bloom. Polar blooms

represent a relevant fraction of the carbon production in some regions of the world, such as the Ross Sea and the Weddell Sea in Antarctica, and the Barents Sea in the Arctic. If the rate of melting is high and the stratification is low, the sea ice biomass may rapidly sink to the bottom of the ocean and likely become a sink for the atmospheric CO_2 . In both cases, the size and weight of the organisms affect the sinking velocity, together with the grazing rate by zooplankton.

Most Arctic and Antarctic marine species depend upon the presence of sea ice [1]. The polar marine food chain begins with ice algae that cling within and to the underside of the dark ice pack all winter and creates a dense mat within and under the ice with the end of the long darkness in spring. Once sea ice has almost completely melted away, a phytoplankton bloom develops in the water beneath the ice, spreading for dozen of kilometers, surrounding the ice edge. This highly productive ice-edge ecosystem is home to numerous crustaceans and other invertebrates. These in turn are eaten by fish species. Organic material released from the ice algae mat and the phytoplankton bloom enriches the sea floor, also supporting a benthic (sea bottom) community of shellfish and other invertebrates. Unique among the world's ecosystems, the ice-edge zone moves thousands of kilometers each year, north in spring and south in fall in the northern hemisphere and viceversa in the southern hemisphere. Walrus, penguins, numerous species of seals and cetaceans follow the ice-edge, taking advantage of the ready access to food, mating and raising pups. Seals are also in turn preyed on by polar bears in the Arctic.

In a global warming scenario, the almost complete elimination of multi-year ice in the Arctic Ocean and the thinning or disappearing of seasonal sea ice in both hemispheres are



likely to be immensely disruptive to all the ice-dependent microorganisms, which will lack a permanent habitat. And consequently, all the polar food chains may be disrupted.

Sea ice biota has been studied for over few decades. Few regions have been highly characterized, but sea ice biological variability at different temporal and spatial scales is still lacking. Sea ice is one of the largest ecosystem on earth, but is also one of the less sampled: sampling sea ice biota is in fact not an easy task. It is costly and time-consuming and often it is done in severe environmental conditions. In absence of data and remote sensing facilities, modelling can give a large contribution to the understanding of the sea ice ecosystem, as well as it can provide the wider picture of its qualitative and quantitative importance, which is still missing.

SEA ICE ECOSYSTEM MODELLING: STATE-OF-THE-ART

To date, very few studies have dealt with modelling of coupled sea ice algae with phytoplankton production and most of the studies usually concerned one or the other subject.

[5, and following developments] are the only ones, to date, that have developed a comprehensive fast-ice ecosystem model and applied it to the Antarctic sea ice. They coupled a simple first-year sea ice thermodynamic model with an intermediate complexity model of microalgal growth. The biological component was based on a maximum temperature-dependent algal growth rate, which was reduced by light or nutrient insufficiency or suboptimal salinity. However, they applied the model in a landfast sea ice region that differs in many aspects from pack ice areas, where internal communities are generally relict of the previous year bottom communities and can strongly contribute to

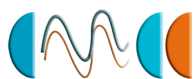
the overall biomass. They also did not consider the presence of surface communities, locally common in Antarctic where heavy snow loads cause seawater flooding at the snow-ice interface.

[6] and [7] simplified the physics of the one-dimensional model of [5] to produce a quasi three-dimensional model to investigate the temporal and large-scale horizontal variation in standing stock and rates of primary production of ice algae in the Southern Ocean. However, productivity was allowed only in a prescribed interfacial layer of 0.02 m at the ice-snow interface and in a prescribed freeboard layer of 0.1 m, while sea ice bottom communities were not considered.

[21] developed an ice-ocean ecosystem model and applied it to Lake Saroma, in the bottom 0.02 m of sea ice. They used a 10-layer Maykut-Untersteiner thermodynamic sea ice model, 1-D vertical equations for heat, salinity and momentum with the turbulent closure scheme of [17] and an intermediate complexity ecosystem model, made of two submodels: a pelagic one with 13 compartments and an ice one with 12 compartments. Their objective was to develop a system representing the exchange of organic matter between the ice and water components, including both the vertical and the lateral variations.

[16] developed a 1-D ice-ocean ecosystem model to determine the factors controlling the bottom-ice algal community (0.02 m) of the landfast ice off Barrow, Alaska. Snow and ice data were provided from observations.

[18] developed a simplified version of the ice algae model of [5] but considered more physical processes. The authors aimed to investigate the importance of different limiting factors, such as light, nutrients and ice growth rate on ice algal growth and decline and on biomass



accumulation. However, also [18] considered the algae to grow in a prescribed fraction of sea ice: the bottom 0.02 m only.

We present here a novel model for simulating sea ice biology, BFM-SI. It is directly derived from an already existing and comprehensive biogeochemical model of the ocean (BFM, [35]), which will be shortly reviewed. The first implementation focuses on primary producers, which are the most abundant group of organisms found in sea ice and the most relevant group in terms of export of biomass to the ocean. The biogeochemical equations of the sea ice algae dynamics are here rewritten after BFM, according to the nomenclature associated to the new chosen functional groups. In order to ensure total mass conservation, BFM-SI is also fully coupled to a simplified version of the standard BFM. All the fluxes of dissolved and particulate inorganic and organic matter at the boundaries with the ocean and with the atmosphere are described. This work concludes with an outlook on the potentialities of BFM-SI for large-scale applications.

BFM: A SHORT REVIEW

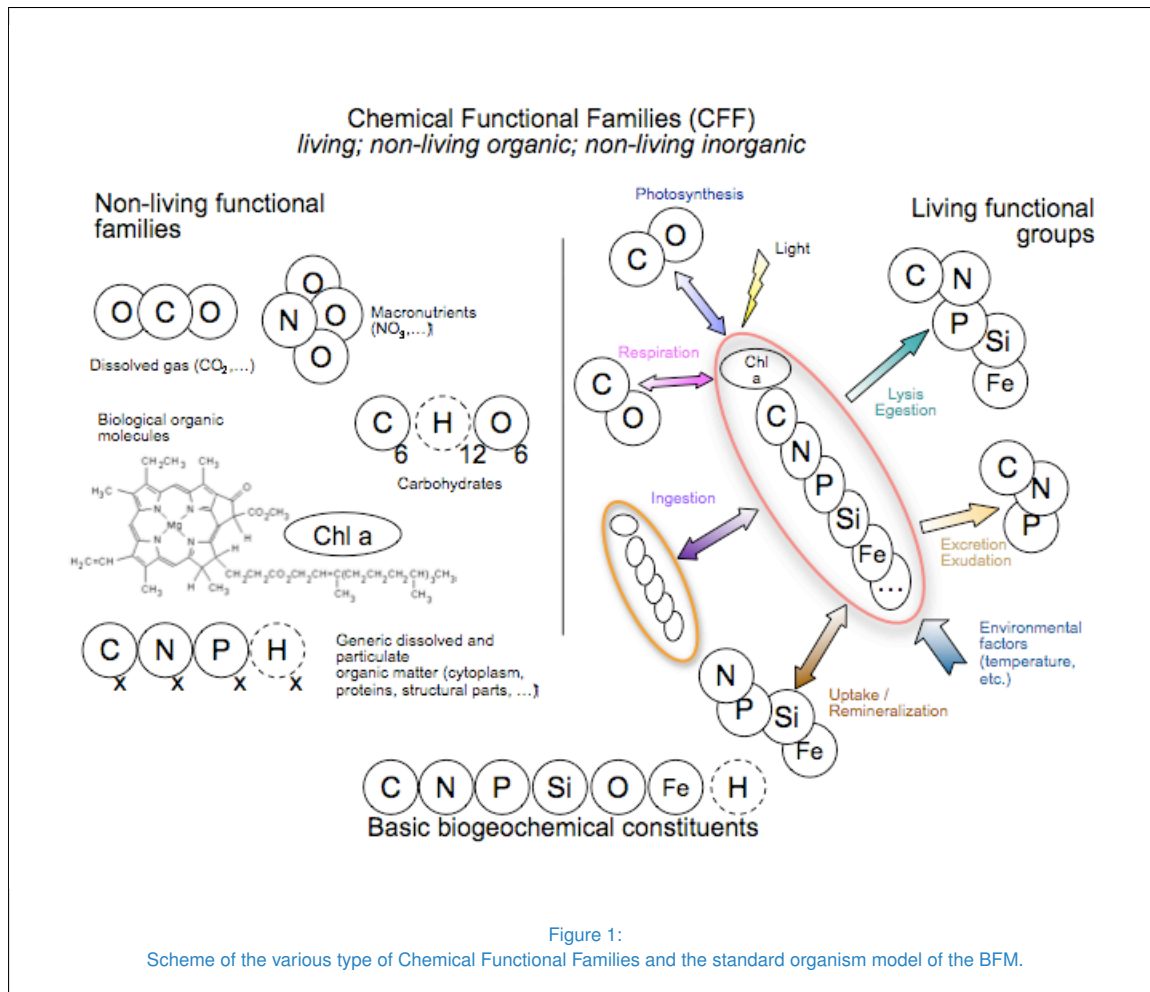
The Biogeochemical Flux Model (BFM, <http://bfm.cmcc.it>, [35, 32]) is a direct descendant of the European Regional Seas Ecosystem Model (ERSEM I and ERSEM II, [8, 9]), which was the first comprehensive model to include physiological considerations in the definition of the divergence of material fluxes. The model has been widely used by the scientific community in coastal and regional seas [26, 3, 37, 38, 22, 2, 23, 36, 24] as well as in climate studies [27, 33] and in a global ocean coupled physical-biogeochemical numerical application (PELAGOS, PELAgic biogeochemistry model for Global Ocean Simulations, [32]). The BFM generalizes the biogeochemical concepts developed in ERSEM, elucidating the basic

constituents, introducing a clear definition of the ecosystem state variables and adding new important biogeochemical constituents such as iron and chlorophyll.

The BFM is written in terms of a functional group approach with a new formalism that is based on the conceptual framework of Chemical Functional Families (CFF) and Living Functional Groups [35]. The core components of the formalism are the CFFs (Fig. 1) which are theoretical constructs that are useful to describe the way materials are exchanged in marine biogeochemistry. CFFs can be described in terms of concentrations, which are measurable quantities in the limits of laboratory or in situ experiments. CFFs are divided in inorganic, non-living organic and living organic compounds (Fig. 1) and they are measured in equivalents of major chemical elements (C, N, P, Si, O, Fe) or in molecular weight units as in the case of chlorophyll. Members of one LFG are represented by the prototype of a standard organism as in Fig. 1. The standard organism is thus the model of the LFGs, whose total biomass is composed of living CFFs and interacts with other (living and non-living) CFFs by means of universal physiological and ecological processes such as photosynthesis, excretion, grazing, etc. The mathematical relationships between the CFFs and the LFG functionalities are defined following the stoichiometrical requirements of basic elements, which are dynamically varying between given maximum and minimum values of element ratios.

The BFM standard configuration in the pelagic system resolves totally 54 state variables derived from:

- 4 different LFGs for phytoplankton (diatoms, autotrophic nanoflagellates, picophytoplankton and large phytoplankton)
- 4 LFGs for zooplankton (omnivorous and



Source: [35], <http://bfm.cmcc.it>

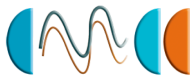
carnivorous mesozooplankton, microzooplankton and heterotrophic nanoflagellates)

- 1 LFG for bacteria
- 9 inorganic CFFs for nutrients and gases (phosphate, nitrate, ammonium, silicate, dissolved iron, reduction equivalents, oxygen, carbon dioxide and dissolved inorganic carbon)
- 4 organic non-living CFFs for dissolved and particulate detritus.

THE BFM-SI IMPLEMENTATION

The new implementation of a sea ice system in the framework of the BFM is directly derived from its theoretical basis. As a first implementation, the system is highly simplified and the chosen CFFs and LFGs are reduced. However, more subgroups may be easily included in future developments.

The new implementation (BFM-SI, Fig. 2) takes advantage of the same biological processes of the pelagic BFM. The focus is here on primary producers, which are assumed to differently adapt and acclimatize to the new physical



environment. The main differences between BFM and BFM-SI stand in the type and number of CFFs and LFGs (Table 1), in the parameters assigned to several physiological and ecological processes (Table 2) and in the dimensional form they represent. While pelagic state variables are expressed in terms of their constituent per cubic meters, the BFM-SI state variables are expressed in terms of constituent per square meters. The strategy of coupling will be further described.

BFM-SI totally resolves 28 state variables (Fig. 2, Table 1) which are derived from the definition of new LFGs and CFFs:

- 2 different LFGs for sea ice algae (adapted diatoms and surviving sea ice algae, mostly represented by autotrophic nanoflagellates)
- 6 inorganic CFFs for nutrients and gases (phosphate, nitrate, ammonium, silicate, oxygen and carbon dioxide)
- 2 organic non-living CFFs for dissolved and particulate detritus
- 1 LFG for a generic group of aerobic and anaerobic sea ice bacteria
- 1 LFG for a generic group of sea ice microzooplankton

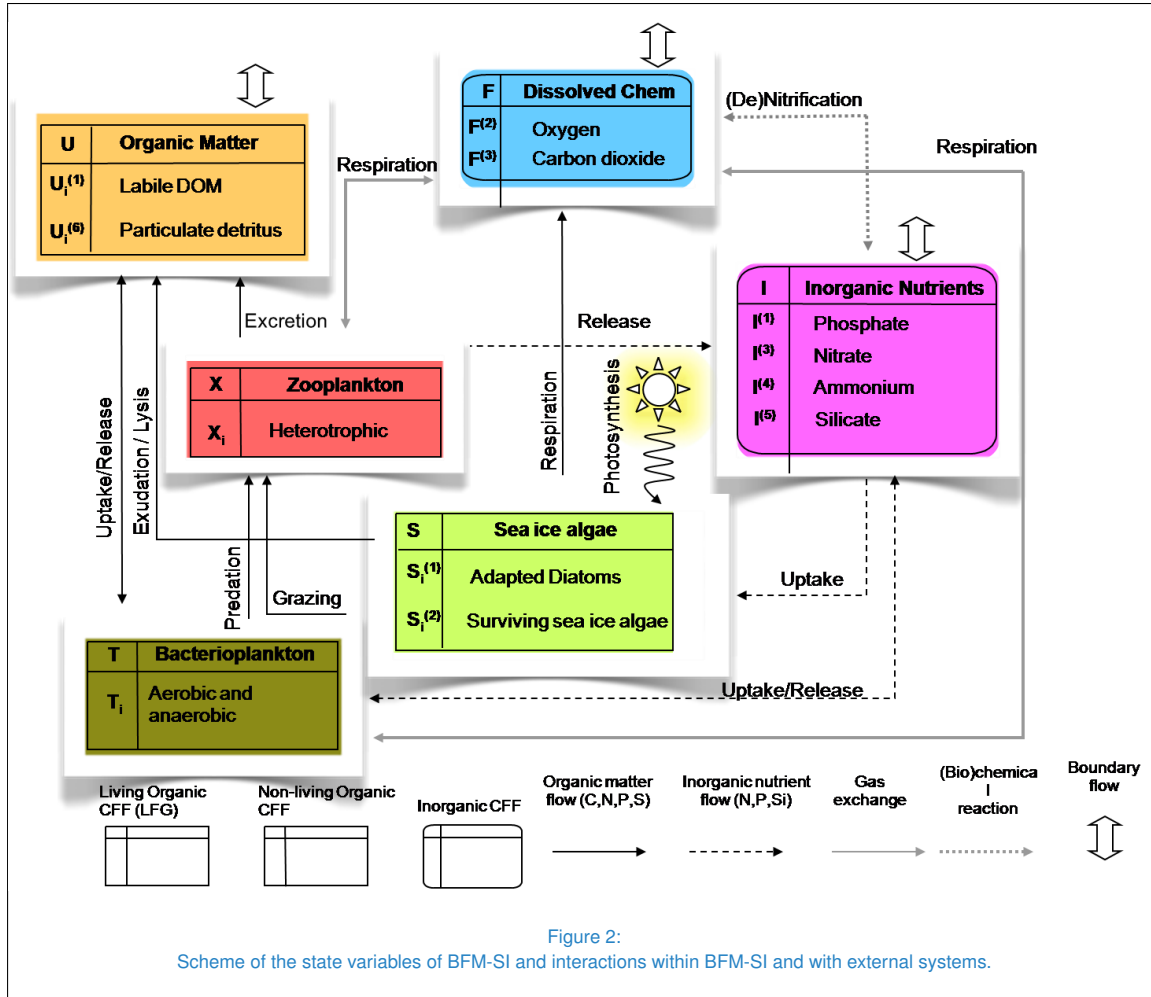
Each state variable interacts with the others through the universal physiological and ecological processes depicted in Fig. 2. BFM-SI already includes parameterizations of sea ice bacteria and zooplankton, which follow the same dynamics as their counterpart in the pelagic BFM. However, those two groups are not currently considered in this first implementation since their role is relatively small and/or not fully understood. Nonetheless, both groups are ready to be included in future more extensive studies.

As for BFM, nitrate is assumed here to be the sum of both nitrite and nitrate. All the nutrient:carbon ratios in chemical organic and LFGs are allowed to vary within their given range and each component has a distinct biological time rate of change. This kind of parametrization is meant to mimic the adaptation of organisms to the diverse availability of nutrients and light observed in nature, and also allow to recycle organic matter depending on the actual nutrient content [8, 34].

SEA ICE ALGAE DYNAMICS

As mentioned earlier, the focus is here on primary producers, while other LFG such as bacteria and zooplankton are not currently considered. As a first implementation of the BFM in sea ice, 2 distinct subgroups have been chosen as representative of sea ice primary producers:

- Adapted diatoms, which are meant to be highly adapted to the environment and also show distinct skills in acclimatize. They are supposed to be first light-limited and, later in the bloom, dependent on nutrient availability. They have an Equivalent Spherical Diameter (ESD) of 20-200 μm and preyed by adult mesozooplankton ($> 200 \mu\text{m}$) and microzooplankton of larger dimensions (20-200 μm), which are not currently present in the sea ice system, but act externally in the pelagic BFM when sea ice melts and algae are released in the water column. Sea ice diatoms are the main source of biogenic silica and differ from the other subgroup being their growth limited by dissolved silicate.
- Surviving sea ice algae, which may be mostly represented by autotrophic nanoflagellates, are meant to only survive in the sea ice environment, being



less adapted to it and showing less possibilities of acclimatization. However, they may be able to grow in sea ice if the diatoms bloom is quickly exhausted - for instance, for depletion of silicate - and a sufficient amount of nutrients is still available for their growth. Their ESD is 2-20 μm and are mainly externally preyed by pelagic microzooplankton.

sis (lys), nutrient uptake (upt), predation (prd) and biochemical synthesis (syn). Both subgroups share the same form of primitive equations, but are differentiated in terms of the values of the physiological parameters (Table 2). There are 5 living CFFs that describe the constituents of the generic variable sea ice algae A (with constituents C, N, P, Si and Chl, see Table 1) and thus for each group we have 4 or

The mathematical notation used here is the same defined for the pelagic BFM and described in [35]. Sea ice algae are involved in several processes: gross primary production (gpp), respiration (rsp), exudation (exu), cell ly-

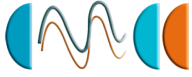


Table 1

List of the Chemical Functional Family state variables (CFF) of BFM-SI.

Variable	Type	Components	Num. of CFFs	Description
$I^{(1)}$	IO	P	1	Phosphate (mmol P m^{-2})
$I^{(3)}$	IO	N	1	Nitrate (mmol N m^{-2})
$I^{(4)}$	IO	N	1	Ammonium (mmol N m^{-2})
$I^{(5)}$	IO	Si	1	Silicate (mmol Si m^{-2})
$F^{(2)}$	IO	O	1	Dissolved oxygen (mg C m^{-2})
$F^{(3)}$	IO	C	1	Carbon dioxide (mg C m^{-2})
$A_i^{(1)}$	LO	C N P Si Chl	5	Adapted diatoms (mg C m^{-2} , $\text{mmol N-P-Si m}^{-2}$, mg Chl-a m^{-2})
$A_i^{(2)}$	LO	C N P Chl	4	Surviving sea ice algae (mg C m^{-2} , mmol N-P m^{-2} , mg Chl-a m^{-2})
T_i	LO	C N P	3	Sea ice bacteria (mg C m^{-2} , mmol N-P m^{-2})
X_i	LO	C N P	3	Sea ice microzooplankton (mg C m^{-2} , mmol N-P m^{-2})
$U_i^{(1)}$	NO	C N P	3	Dissolved organic detritus (mg C m^{-2} , mmol N-P m^{-2})
$U_i^{(6)}$	NO	C N P Si	4	Particulate organic detritus (mg C m^{-2} , $\text{mmol N-P-Si m}^{-2}$)

Legend: IO = Inorganic; LO = Living organic; NO = Non-living organic. The subscript i indicates the basic components of the CFF, e.g. $A_i^{(1)} \equiv (A_c^{(1)}; A_n^{(1)}; A_p^{(1)}; A_s^{(1)}; A_l^{(1)})$.

5 equations:

$$\frac{dA_c}{dt} = \frac{dA_c}{dt} \Big|_{F^{(3)}}^{gpp} - \frac{dA_c}{dt} \Big|_{U_c^{(1)}}^{exu} - \frac{dA_c}{dt} \Big|_{F^{(3)}}^{resp} - \sum_{j=1,6} \frac{dA_c}{dt} \Big|_{U_c^{(j)}}^{lys} \quad (1)$$

$$\frac{dA_n}{dt} = \sum_{j=3,4} \frac{dA_n}{dt} \Big|_{I^{(j)}}^{upt} - \sum_{j=1,6} \frac{dA_n}{dt} \Big|_{U_n^{(j)}}^{lys} \quad (2)$$

$$\frac{dA_p}{dt} = \frac{dA_p}{dt} \Big|_{I^{(1)}}^{upt} - \sum_{j=1,6} \frac{dA_p}{dt} \Big|_{U_p^{(j)}}^{lys} \quad (3)$$

$$\frac{dA_s^{(1)}}{dt} = \frac{dA_s^{(1)}}{dt} \Big|_{I^{(5)}}^{upt} - \frac{dA_s^{(1)}}{dt} \Big|_{U_s^{(6)}}^{lys} \quad (4)$$

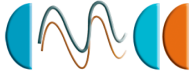
$$\frac{dA_l}{dt} \Big|^{syn} = \theta_{chl} \left(\frac{dA_c}{dt} \Big|_{F^{(3)}}^{gpp} - \frac{dA_c}{dt} \Big|_{U_c^{(1)}}^{exu} \right) - \left(\frac{dA_c}{dt} \Big|_{F^{(3)}}^{resp} + \frac{dA_c}{dt} \Big|_{U_c^{(6)}}^{lys} \right) \frac{A_l}{A_c} \quad (5)$$

where θ_{chl} is the dynamical chl:C ratio (see further).

The rate of change of carbon in sea ice algae depends on gross primary production, exudation, respiration, lysis and predation (Eq. 1). Gross primary production in Eq. 1 is the rate of change of sea ice algae carbon A_c due to photosynthesis, which involves an uptake of dis-

Table 2
Ecological and physiological parameters in BFM-SI.

Symbol	A ⁽¹⁾	A ⁽²⁾	Description
r_0^A	1.5	2.0	Maximum specific photosynthetic rate (d^{-1})
Q_{10}^A	2.0	2.0	Characteristic Q_{10} coefficient (-)
θ_{chl}^0	0.035	0.03	Optimal quatum chl-a:C (mg chl mg C^{-1})
α_{chl}^0	1.8 e^{-3}	3.8 e^{-6}	Maximum light utilization coefficient ($\text{mg C (mg chl)}^{-1} \text{ mE}^{-1} \text{ m}^2 \text{ s}$)
d_s	0.1	-	Half saturation value for Si-limitation (mmol Si m^{-2})
b_A	0.05	0.1	Basal specific respiration rate (d^{-1})
γ_A	0.10	0.10	Activity respiration fraction (-)
β_A	0.05	0.20	Excreted fraction of primary production (-)
$d_A^{p,n,s}$	0.1	0.2	Nutrient stress threshold (-)
d_{OA}	0.1	0.1	Maximum specific lysis rate (d^{-1})
a_1	$2.5 \text{ } 10^{-3}$	$2.5 \text{ } 10^{-3}$	Specific affinity constant for P ($\text{m}^{-2} \text{ mg C}^{-1} \text{ d}^{-1}$)
a_3	$2.5 \text{ } 10^{-3}$	$2.5 \text{ } 10^{-3}$	Specific affinity constant for N- NO_3 ($\text{m}^{-2} \text{ mg C}^{-1} \text{ d}^{-1}$)
a_4	$2.5 \text{ } 10^{-3}$	$2.5 \text{ } 10^{-3}$	Specific affinity constant for N- NH_4 ($\text{m}^{-2} \text{ mg C}^{-1} \text{ d}^{-1}$)
$s_{A(1)}^{opt}$	0.03	-	Standard Si:C ratio in sea ice diatoms (mmol Si mg C^{-1})
$s_{A(1)}^{max}$	0.085	-	Maximum Si:C ratio in sea ice diatoms (mmol Si mg C^{-1})
p_A^{min}	$1.97 \text{ } 10^{-4}$	$1.97 \text{ } 10^{-4}$	Minimum phosphorus quota (mmol P mgC^{-1})
p_A^{opt}	$7.86 \text{ } 10^{-4}$	$7.86 \text{ } 10^{-4}$	Optimal phosphorus quota (mmol P mgC^{-1})
p_A^{max}	$1.57 \text{ } 10^{-3}$	$1.57 \text{ } 10^{-3}$	Maximum phosphorus quota (mmol P mgC^{-1})
n_A^{min}	$3.78 \text{ } 10^{-4}$	$3.78 \text{ } 10^{-4}$	Minimum nitrogen quota (mmol N mgC^{-1})
n_A^{opt}	$1.26 \text{ } 10^{-3}$	$1.26 \text{ } 10^{-3}$	Optimal nitrogen quota (mmol N mgC^{-1})
n_A^{max}	$2.52 \text{ } 10^{-3}$	$2.52 \text{ } 10^{-3}$	Maximum nitrogen quota (mmol N mgC^{-1})
c_A	10.0 e^{-3}	10.0 e^{-3}	Specific absorption coefficient for chlorophyll- <i>a</i> ($\text{m}^2 (\text{mg Chl-}a)^{-1}$)
c_U	0.1 e^{-3}	0.1 e^{-3}	Specific absorption coefficient for detritus contribution to extinction ($\text{m}^2 (\text{mg C})^{-1}$)
Ω_c^o	$\frac{1}{12}$	$\frac{1}{12}$	Unit converison factor and stoichiometric coefficient ($\text{mmmolO}_2 \text{ mgC}^{-1}$)



solved carbon dioxide $F^{(3)}$. It is written as:

$$\left. \frac{dA_c}{dt} \right|_{F^{(3)}}^{gpp} = f_A^T f_A^E f_A^s r_A^0 A_c \quad (6)$$

where the r_A^0 is the maximum specific photosynthetic rate under nutrient-replete, light saturated conditions (Table 2). The f functions are multiplicative, non-dimensional regulating factors for temperature, light and silicate, which vary from 0 to 1.

Temperature is regulating several physiological processes. Its effect is expressed in a non-dimensional form by f_A^T :

$$f_A^T = Q_{10}^{A \frac{T-10}{10}} \quad (7)$$

where Q_{10}^A is the characteristic doubling temperature parameter (Table 2).

Many relevant biological processes, such as potential photosynthesis, are also affected by the non-dimensional light regulating factor f_A^E :

$$f_A^E = 1 - \exp\left(-\frac{E_{PAR}}{E_K}\right) \quad (8)$$

where E_{PAR} is the Photosynthetic Available Radiation (PAR). E_{PAR} is parametrized according to the Lambert-Beer formulation with depth-dependent extinction coefficients:

$$E_{PAR}(z) = \varepsilon_{PAR} F_{sw} e^{(\lambda_s + \lambda_i)z + \int_z^0 \lambda_{bio}(z') dz'} \quad (9)$$

where F_{sw} is the short-wave surface irradiance flux and may be derived from data or from a coupled physical model, such as the one of [28, 29]. The irradiance flux is then converted by BFM-SI from $W m^{-2}$ to the units of $\mu E m^{-2} s^{-1}$ with the constant factor 1/0.215 [25]. ε_{PAR} is the coefficient determining the portion of PAR in F_{sw} . Light propagation takes into account the extinction due to the background extinction of snow/sea ice $\lambda_{s,i}$ and due to particles in the sea ice λ_{bio} , where:

$$\lambda_{bio} = \sum_j^2 c_A A_l^{(j)} + c_{U(6)} U_c^{(6)}. \quad (10)$$

Thus, λ_{bio} takes into consideration the extinction due to sea ice algae chlorophyll and to particulate detritus, while dissolved substances and other inorganic matter are not currently taken into account. The c_A and c_U constants are the specific absorption coefficients of each suspended substance (Table 2).

E_K is the light saturation parameter, that is the ratio between the maximum chl-*a* specific photosynthetic rate and the maximum light utilization coefficient, i.e.:

$$E_K = \frac{P_m^*}{\alpha^*}. \quad (11)$$

As for pelagic phytoplankton of BFM:

$$P_m^* = f_A^T f_A^s r_A^0 \frac{A_c}{A_l} \quad (12)$$

$$\alpha^* = f_A^T f_A^s \alpha_{chl}^0 \quad (13)$$

where f_A^T is the regulating factor for temperature, f_A^s is the regulating factor for silicate, r_A^0 is the maximum specific photosynthetic rate under nutrient-replete, light-saturated conditions and α_{chl}^0 is the maximum slope of the production-irradiance curve at optimal conditions (Table 2).

The f_A^s is parametrized as an external limiting factor with a Michaelis-Menten form:

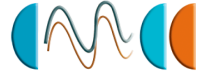
$$f_A^s = \frac{I^{(5)}}{I^{(5)} + d_s} \quad (14)$$

where d_s is the Michaelis-Menten constant for SiO_2 uptake inhibition (Table 2).

The exudation rate of Eq. 1 reads:

$$\left. \frac{dA_c}{dt} \right|_{U_c^{(1)}}^{exu} = [\beta_A + (1 - \beta_A)(1 - f_A^{n,p})] \left. \frac{dA_c}{dt} \right|_{F^{(3)}}^{gpp} \quad (15)$$

where β_A is a constant fraction of carbon uptake (Table 2) and $f_A^{n,p}$ is a Liebig-like regulating



factor for internal nutrient ratio:

$$f_A^{n,p} = \min \left(\frac{A_n/A_c - n_A^{min}}{n_A^{opt} - n_A^{min}}, \frac{A_p/A_c - p_A^{min}}{p_A^{opt} - p_A^{min}} \right) \quad (16)$$

where $n(p)_A^{opt}$ is the nitrate(phosphate) optimal ratio, while $n(p)_A^{min}$ is the nitrate(phosphate) minimum quota (Table 2).

The respiration rate of Eq. 1 is written as:

$$\gamma_A \left(\frac{dA_c}{dt} \Big|_{F^{(3)}}^{rsp} - \frac{dA_c}{dt} \Big|_{U_c^{(1)}}^{exu} \right) = f_A^T b_A A_c + \quad (17)$$

where f_A^T is the metabolic regulating factor for temperature, b_A is a constant specific rate of respiration and γ_A is a fraction of the assimilated production (Table 2).

The loss of carbon via lysis of Eq. 1 is written as:

$$\sum_{j=1,6} \frac{dA_c}{dt} \Big|_{U_c^{(j)}}^{lys} = \frac{1}{f_A^{p,n} + d_A^{p,n}} d_{O_A} A_c \quad (18)$$

where $d_A^{p,n}$ is the nutrient stress threshold and d_{O_A} is the maximum specific lysis rate (Table 2).

The chlorophyll rate of change of Eq. 5 is due to chlorophyll synthesis. The net chlorophyll synthesis is a function of acclimation to light conditions, nutrient availability and turnover rate. As in BFM, it is assumed that nutrient-stressed cells releasing substantial amounts of dissolved organic carbon tend to regulate their internal chl:C ratio in order to avoid unconstrained decreases.

The rate of change of net photosynthesis is thus primarily controlled by the dynamical chl:C ratio θ_{chl} proposed by [13], which regulates the

amount of chl-*a* in the cell according to a non-dimensional ratio between the realized photosynthetic rate in Eq. 5 and the maximum potential photosynthesis, i.e.:

$$\theta_{chl} = \theta_{chl}^0 \frac{f_A^E r_A^0 A_c}{\alpha_{chl}^0 E_{PAR} A_l} \quad (19)$$

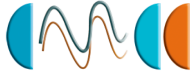
where θ_{chl}^0 is the maximum quatum chl-*a*:C and α_{chl}^0 is the maximum slope of the production-irradiance curve at optimal growth conditions (Table 2). The same considerations about down-regulation and chlorophyll losses as detailed in [35] for phytoplankton are valid for sea ice algae.

NUTRIENT SUPPLY AND DYNAMICS

Nutrients supply for algal growth comes from the mixed layer up to the ice sheet for sustaining bottom communities, but also from snow deposition through brine drainage for surface communities and from *in situ* regeneration processes.

Even in isolated brine pockets, bacteria, heterotrophic protozoa and small metazoans have been shown to regenerate the major nutrients [4], but not silicate. Silicate dissolution and regeneration may be slower than demand and can be the major limiting factor for diatoms growth [20], shifting the community from being diatom-dominated to flagellates-dominated [11]. The slow regeneration of silicate in sea ice is parametrized in BFM-SI as a smaller value for the half saturation of silica and a larger value for the standard Si:C quatum in adapted diatoms (Table 2).

The boundary fluxes are currently added as additional source terms to the biogeochemical equations and solved explicitly. For instance, in the case of an inorganic nutrient in sea ice (e.g. nitrate, $I^{(3)}$), the complete equation is written



as

$$\frac{dI^{(3)}}{dt} = \frac{dA_n^{(1)}}{dt} \Big|_{I^{(3)}}^{upt} + \frac{dA_n^{(2)}}{dt} \Big|_{I^{(3)}}^{upt} + \frac{dI^{(3)}}{dt} \Big|_{N^{(3)}}^{flux} \quad (20)$$

where the first two terms on the right hand side represent the uptake from sea ice algae and the last one is the flux of nutrient at the boundaries. The external mechanisms of nutrients replenishment (exchange with the ocean and atmospheric deposition) will be analyzed in the next sections.

The uptake of nitrogen and phosphorous by algae (Eq. 20) is regulated by a Droop kinetics:

$$\sum_{i=3,4} \frac{dA_n}{dt} \Big|_{I^{(i)}}^{upt} = \min \left(\left(a_A^3 I^{(3)} + a_A^4 I^{(4)} \right) A_c, n_A^{opt} G_A + f_A^T r_A^0 \left(n_A^{max} - \frac{A_n}{A_c} \right) A_c \right) \quad (21)$$

$$\frac{dA_p}{dt} \Big|_{I^{(1)}}^{upt} = \min \left(a_A^1 I^{(1)} A_c, p_A^{opt} G_A + f_A^T r_A^0 \left(p_A^{max} - \frac{A_p}{A_c} \right) A_c \right) \quad (22)$$

where the a constants are the membrane affinity for nitrate, ammonium and phosphate (Table 2).

The uptake of silicate is, instead, only function of the maximum Si:C ratio $s_{A^{(1)}}^{max}$ and of the net production $G_{A^{(1)}}$ of Eq. 1:

$$\frac{dA_s}{dt} \Big|_{I^{(5)}}^{upt} = s_{A^{(1)}}^{max} G_{A^{(1)}} \quad (23)$$

Whenever sea ice algae carbon is lost by lysis, a proportional loss is found for algae nutrient content and is distributed between a dissolved and a particulate fraction ([35]). For instance,

the equations of the lysis rate for phosphorous are:

$$\frac{dA_p}{dt} \Big|_{U_p^{(6)}}^{lys} = p_A^{min} \frac{\partial A_c}{\partial t} \Big|_{U_c^{(6)}}^{lys} \quad (24)$$

$$\frac{dA_p}{dt} \Big|_{U_p^{(1)}}^{lys} = \frac{A_p}{A_c} \sum_{j=1,6} \frac{\partial A_c}{\partial t} \Big|_{U_c^{(j)}}^{lys} - \frac{\partial A_p}{\partial t} \Big|_{U_p^{(6)}}^{lys} \quad (25)$$

Silicate is instead only released in particulate form:

$$\frac{\partial A_s^{(1)}}{\partial t} \Big|_{U_s^{(6)}}^{lys} = \frac{A_s^{(1)}}{A_c^{(1)}} \frac{\partial A_c^{(1)}}{\partial t} \Big|_{U_c^{(6)}}^{lys} \quad (26)$$

GASES AND DETRITUS

The following equations are derived by combining terms from the previous sections in order to ensure mass conservation. The net production of oxygen is due to the gross primary production and to algae respiration rates:

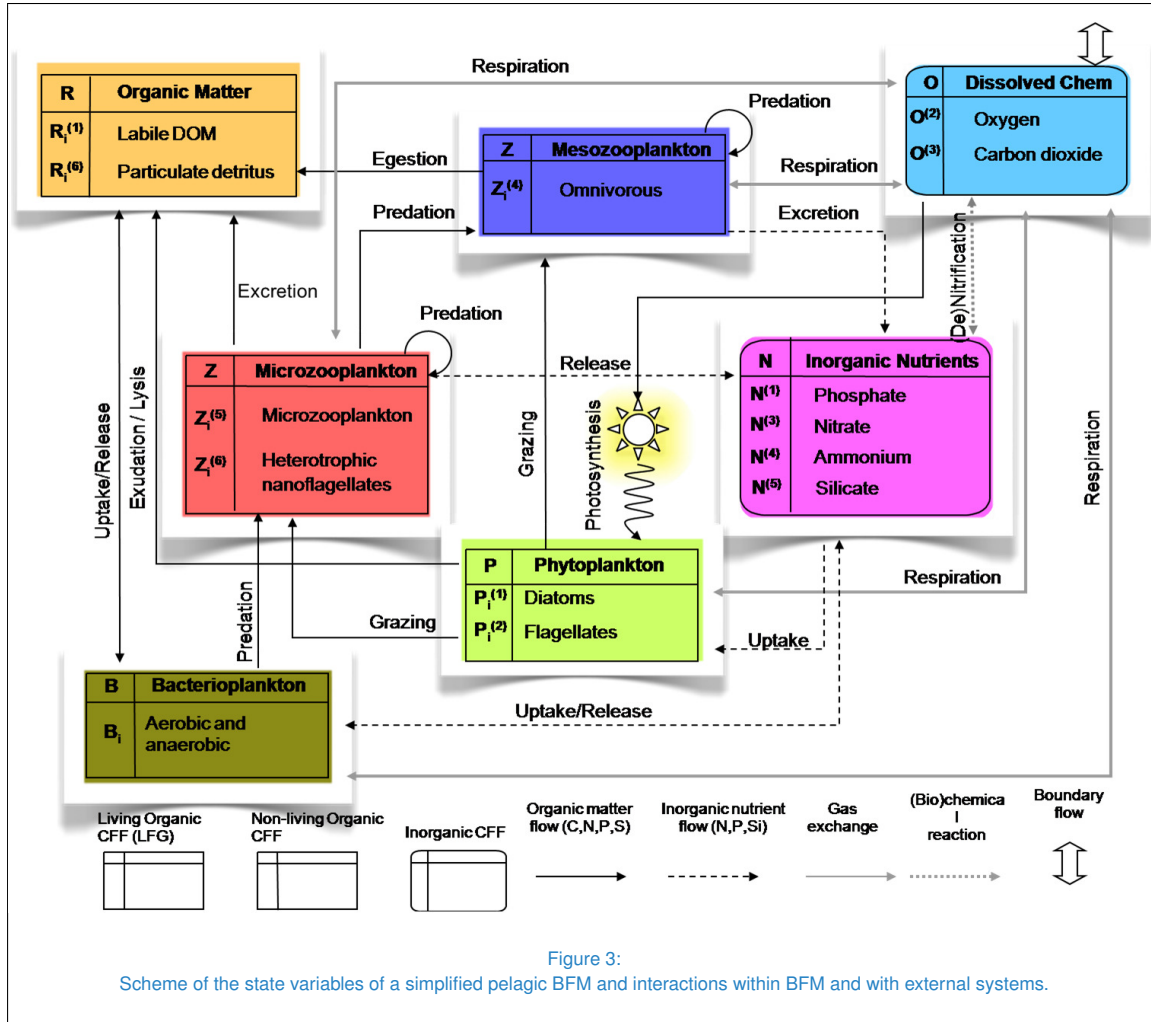
$$\frac{\partial F^{(2)}}{\partial t} \Big|_{bio} = \Omega_c^o \sum_{j=1}^2 \left(\frac{\partial A_c^{(j)}}{\partial t} \Big|_{F^{(3)}}^{gpp} - \frac{\partial A_c^{(j)}}{\partial t} \Big|_{F^{(3)}}^{rsp} \right) \quad (27)$$

where Ω_c^o is the stoichiometric conversion factor to oxygen units in respiration and photosynthesis (Table 2).

Dissolved organic matter (DOM, $U_i^{(1)}$ in BFM-SI) is a non-living functional group including C, N and P constituents. In this current implementation, DOM is produced by sea ice algae (Eq. 15), though in the complete setup shown in Fig. 2, DOM will be produced also by sea ice bacteria and microzooplankton:

$$\frac{\partial U_c^{(1)}}{\partial t} \Big|_{bio} = \sum_{j=1}^2 \frac{\partial A_c^{(j)}}{\partial t} \Big|_{U_c^{(1)}}^{exu} \quad (28)$$

$$\frac{\partial U_i^{(1)}}{\partial t} \Big|_{bio} = \sum_{j=1}^2 \frac{\partial A_i^{(j)}}{\partial t} \Big|_{U_i^{(1)}}^{exu} \quad i = n, p. \quad (29)$$



Particulate organic matter (POM, $U_i^{(6)}$ in BFM-SI) is made of C, N, P and Si:

$$\left. \frac{\partial U_c^{(6)}}{\partial t} \right|_{bio} = \sum_{j=1}^2 \left. \frac{\partial A_c^{(j)}}{\partial t} \right|_{U_c^{(6)}}^{lys} \quad (30)$$

$$\left. \frac{\partial U_i^{(6)}}{\partial t} \right|_{bio} = \sum_{j=1}^2 \left. \frac{\partial A_i^{(j)}}{\partial t} \right|_{U_i^{(6)}}^{lys} \quad i = n, p, s \quad (31)$$

where the silicate component of POM is only valid for the release of sea ice diatoms frustules.

THE COUPLING STRATEGY

The construction of a biological system in sea ice implies the coupling with the underlying bi-

ology of the ocean. BFM-SI is in fact coupled to a simplified version of the BFM representing pelagic lower trophic levels in a surface layer of ice-covered oceans (Fig. 3). The standard pelagic BFM has been simplified in a way that every sea ice LFG and CFF has its own pelagic counterpart and there is no loss of material between the two systems (Fig. 4). The number of CFF and LFG is reduced and the total number of state variables computed are 34. The included groups and subgroups in the pelagic BFM are:

- 2 LFGs for phytoplankton (diatoms and autotrophic nanoflagellates)

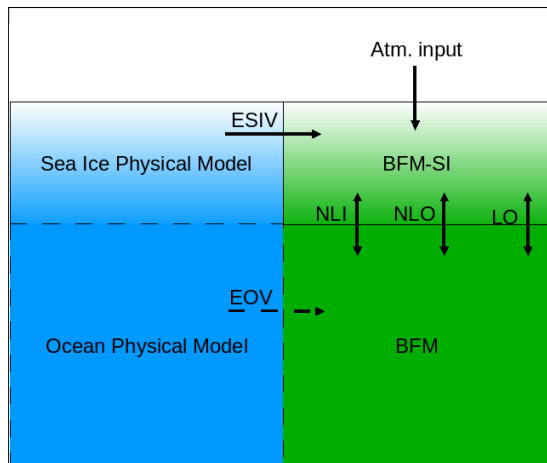
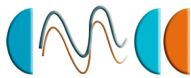


Figure 4:

Structure of the current coupling between physics and biogeochemistry (boxes with continuous line). The sea ice physical model passes offline the Environmental Sea Ice Variables (ESIV) to BFM-SI. BFM-SI is online coupled to BFM through the exchange of Non Living Inorganic (NLI), Non Living Organic (NLO) and Living Organic (LO) matter. Boxes with dashed lines represent the possibility for the sea ice physical model to be also coupled to an ocean physical model, which would pass the Environmental Ocean Variables (EOV) to BFM.

- 3 LFGs for zooplankton (omnivorous mesozooplankton, microzooplankton and heterotrophic nanoflagellates)
- 1 LFG for bacteria
- 9 inorganic CFFs for nutrients and gases (phosphate, nitrate, ammonium, silicate, oxygen, carbon dioxide)
- 2 organic non-living CFFs for dissolved and particulate detritus.

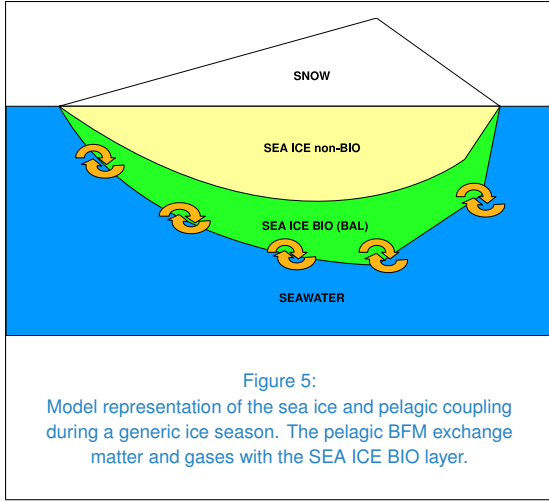
Differently to BFM-SI, the pelagic zooplankton includes 3 different subgroups and mesozooplankton may effectively control the fate of the sea ice algae released into the water and the magnitude of the phytoplankton bloom. Consequently, the diversity of feeding behaviors of zooplankton is maintained.

The exchange of matter between the ocean system and the sea ice system will be the subject of the next section. We focus here on the coupling strategy. BFM-SI has been built as a layer model, in a similar way as the benthic component of BFM is designed. A layer model means that the model is two-dimensional (concentrations are expressed in units of mass per square meters): all the members of a generic layer of the system, as for instance the benthic oxic layer, have to be thought as their constituents are homogeneously distributed on a stratum at the interface with the ocean. However, the state variables of the pelagic BFM are expressed as concentrations in a volume of sea water. The thickness of the considered layer is taken into account in order to have every CFF of both systems (pelagic and benthic) in the same units per cubic meters. This concept can be applied also to the coupling between BFM and BFM-SI, considering that the sea ice biology is distributed in a certain layer of sea ice (the sea ice bio, BAL of Fig. 5). The thickness of the layer can be prescribed, as it has been done previously by [6, 7, 21, 18, 16], or it can be computed by a physical model, such as the one developed by [28, 30], which is a time-varying layer whose thickness depends on the physical properties of sea ice (temperature, salinity and brine volume).

BOUNDARY FLUXES: THE SEA ICE-OCEAN INTERFACE

The major exchanges between the sea ice and the pelagic systems are the fluxes of organic and inorganic matter at the interface. Ice structure determines the porosity and therefore the rate of exchange: frazil ice is less porous than congelation ice and algae may experience, for instance, nutrient depletion in the former.

The rates of advection and diffusion of dissolved and particulate substances from seawater



Source: [30]

ter into the porous bottom layer of ice may also depend on under-ice current velocities, tides and atmospheric pressure cycles [10]. Additionally, high algal biomass in the platelet layer has been found to reduce the flux of nutrients to algae communities of the upper congelation layer in Antarctica [20].

High biomass is usually found in area of slow ice growth rate [19]. During the growth season, convection in the skeletal layer enhances nutrient fluxes [10]. During the melting season, the supply of freshwater increases the stratification just below the ice and reduces the flux of nutrients upward by reducing mixing and friction velocity [14]. Even if the enlargement and interconnections of the brine channels allows a greater biomass accumulation and nutrient supply, it also leads to an increase in the biological loss by cells sinking in the water column.

It is assumed here that the entrapment of dissolved matter follows the same partitioning of salt in sea ice, that is the dynamics of dissolved constituents is treated as the salinity dynamics, as proposed by [28], considering the concentration of dissolved matter in seawater and sea ice growth rate.

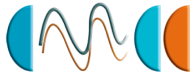
Fluxes are defined positive upward, i.e. towards sea ice in Fig. 4. The nitrate flux is described here as an example of an inorganic nutrient exchange. The flux is composed of a positive part (entrapment) during sea ice formation when sea ice growth is positive, and of a negative part during the melting phase:

$$\left. \frac{dI^{(3)}}{dt} \right|_{N^{(3)}}^{flux-oce} = \max \left(0, \frac{\partial h_i}{\partial t} \right) \cdot \max \left(0, N^{(3)} - \frac{I^{(3)}}{h_{bio}} \right) + \min \left(0, \frac{\partial h_i}{\partial t} \right) \frac{I^{(3)}}{h_{bio}} \quad (32)$$

where $N^{(3)}$ is the nitrate concentration in seawater, h_i is the ice thickness and h_{bio} is the thickness of the biologically active layer in sea ice. When ice starts melting (the last term in the equation above), the release to the water column depends only on the sea ice melting rate and on the sea ice concentration. The same flux, converted into units of volume concentration, is included with opposite sign in the dynamical equation for pelagic nutrients.

The entrapment of particulate matter is assumed to be only a function of the seawater concentration, the sea ice growth rate and the actual available space in the sea ice matrix (brine volume, V_{bio}), while the release during the melting phase is parametrized as function of the sea ice melting rate and sea ice concentrations, as in Eq. (32). For instance, the flux of the chlorophyll component of sea ice algae $A_l^{(1)}$, from the pelagic variable $P_l^{(1)}$ to sea ice is defined as:

$$\left. \frac{dA_l^{(1)}}{dt} \right|_{P^{(1)}}^{flux-oce} = \max \left(0, \frac{\partial h_i}{\partial t} \right) P_l^{(1)} V_{bio} + \min \left(0, \frac{\partial h_i}{\partial t} \right) \frac{A_l^{(1)}}{h_{bio}}. \quad (33)$$



16

BOUNDARY FLUXES: THE SEA ICE-ATMOSPHERE INTERFACE

Nutrient content in snow and liquid precipitation may directly lead to additional nutrient availability for surface communities, and indirectly to internal and bottom communities, and finally to surface waters once sea ice has totally melted away. In the Baltic Sea, for instance, 5% of the total annual flux of N and P and 20–40% of lead and cadmium are deposited as snow: due to the intense stratification of most of the Baltic waters, sea ice is the major source of nutrients and trace elements to the surface Baltic waters during the melting season [15].

The physical processes responsible of the bioavailability of atmospheric nutrients to the sea ice community are snow ice formation and snow flushing. When snow ice forms the fraction of snow that mixes with flooding seawater may bring an additional source of nutrients for internal communities, while during snow flushing episodes the accumulated nutrients in the melting snow may become available also for bottom communities, if brines are permeable. This latter process is the one that it is currently considered in the model for the parametrization of the flux of atmospheric nutrients to bottom sea ice, as shown in Fig. 4. Phosphate and nitrogen concentration in snow may be derived from an atmospheric model or may be prescribed using available observations. The flux of nutrients due to precipitation becomes then a linear function of the snow melting rate, similarly to the flux of matter from sea ice to the ocean during melting of sea ice, i.e. for nitrate:

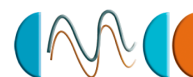
$$\left. \frac{dI^{(3)}}{dt} \right|_{N^{snow}}^{flux-atm} = \min \left(0, \frac{\partial h_s}{\partial t} \right) N^{snow} \quad (34)$$

where N^{snow} is the nitrate concentration in snow and h_s is the snow thickness.

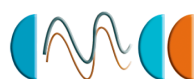
CONCLUSIONS

A novel parameterization of sea ice biogeochemical processes in the frame of an already existing and comprehensive biogeochemical flux model (BFM) has been presented. The new biogeochemical flux model in sea ice (BFM-SI) is directly derived from the BFM formalism and takes the advantage to include the same, already developed and tested, dynamics for lower functional group processes. The new model is coupled to a pelagic counterpart in the ocean, holding the same functional groups except for zooplankton, which, differently from sea water, is size-limited in sea ice.

BFM-SI is the first sea ice biomass-based ecosystem model of higher complexity. It may be used for process-studies, as well as for supporting mesocosm experiments. Currently, BFM-SI is already used to simulate the sea ice biology of a time-varying layer of sea ice, the Biologically-Active Layer of [28, 30] (see also Fig. 5), in 1D numerical studies. Nonetheless, BFM-SI also shows higher potentialities for regional and global applications. BFM-SI has been built in the same modular way as BFM was originally built. Hence, it can be coupled with multi-dimensional physical models. The physical model would define the spatial properties of the system and pass the relevant information, such as temperature, salinity and available light, to BFM-SI. The coupling with a complete physical model of the ocean, as represented in Fig. 4, may allow to properly study the influence of mixed layer depth on nutrient transports through the sea ice interface. Also, the study on the contribution and fate of the sea ice biomass is an important issue with large scale implications. A well-defined picture on the role and magnitude of the sea ice contribution to the bulk of pelagic organic matter is still missing. BFM-SI in coupled configuration with a 3-D physical model of the ocean may contribute to

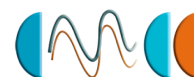


the understanding of the pelagic-sea ice coupling, and may provide adequate estimates of the role and magnitude of the sea ice biomass in the global carbon cycle.

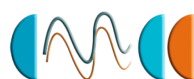


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